

WO 00/15803

PCT/GB99/03048

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## SEQUENCE LISTING

## 5 (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: ACTINOVA LIMITED  
 (B) STREET: 5 Signet Court, Swanns Road  
 10 (C) CITY: Cambridge  
 (E) COUNTRY: United Kingdom  
 (F) POSTAL CODE (ZIP): CB5 8LA

## (ii) TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN

15 (iii) NUMBER OF SEQUENCES: 22

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
 20 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (v) CURRENT APPLICATION DATA:

25 APPLICATION NUMBER: GB N/A

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- 40 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..246

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45 ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA	48
Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu	
1                5                10                15	

50 CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA	96
Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly	
20                25                30	

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	AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA	144
5	Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala	
	35                    40                    45	
	GAA GCT TAC AGA TAT GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT	192
	Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr	
	50                    55                    60	
10	ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT	240
	Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala	
	65                    70                    75                    80	
15	GGA AAA TAA	249
	Gly Lys	

## 20 (2) INFORMATION FOR SEQ ID NO: 2:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 82 amino acids	
	(B) TYPE: amino acid	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
30	Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu	
	1                    5                    10                    15	
	Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly	
	20                    25                    30	
35	Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala	
	35                    40                    45	
	Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr	
40	50                    55                    60	
	Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala	
	65                    70                    75                    80	
45	Gly Lys	

## (2) INFORMATION FOR SEQ ID NO: 3:

50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 228 base pairs	
	(B) TYPE: nucleic acid	

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- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..228

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

15

AAA GAA GAA ACA CCA GAA ACA CCA GAA ACT GAT TCA GAA GAA GAA GTA 48  
Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val  
235 240 245

20

ACA ATC AAA GCT AAC CTA ATC TTT GCA AAT GGA AGC ACA CAA ACT GCA 96  
Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala  
250 255 260 265

25

GAA TTC AAA GGA ACA TTT GAA AAA GCA ACA TCA GAA GCT TAT GCG TAT 144  
Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr  
270 275 280

30

GCA GAT ACT TTG AAG AAA GAC AAT GGA GAA TAT ACT GTA GAT GTT GCA 192  
Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala  
285 290 295

35

GAT AAA GGT TAT ACT TTA AAT ATT AAA TTT GCT GGA 228  
Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
300 305

40

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

50

Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val  
1 5 10 15

Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala  
20 25 30

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Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr  
 35 40 45

5 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala  
 50 55 60

Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
 10 65 70 75

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- 25 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..216

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

30	AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala 80 85 90	48
35	AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly 95 100 105	96
40	ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCA GAT GCA TTA Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu 110 115 120	144
45	AAG AAG GAC AAT GGA GAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr 125 130 135 140	192
	ACT TTA AAT ATT AAA TTT GCT GGA Thr Leu Asn Ile Lys Phe Ala Gly 145	216

50 (2) INFORMATION FOR SEQ ID NO: 6:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
1 5 10 15

15

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
20 25 30

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu  
35 40 45

20

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
50 55 60

25

Thr Leu Asn Ile Lys Phe Ala Gly  
65 70

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(iii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..216

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

45

AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA  
Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
75 80 85

48

50

AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA  
Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
90 95 100

96

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ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCT GAC TTA TTA 144  
Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu  
5 105 110 115 120

GCA AAA GAA AAT GGT AAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT 192  
Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
10 125 130 135

ACT TTA AAT ATT AAA TTT GCT GGA 216  
Thr Leu Asn Ile Lys Phe Ala Gly  
140

15 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
20 (B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

25 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
1 5 10 15

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
30 20 25 30

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu.  
35 40 45

35 Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
50 55 60

Thr Leu Asn Ile Lys Phe Ala Gly  
65 70

40 (2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 216 base pairs  
45 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50 (ix) FEATURE:

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- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..216

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

10	AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala	48
	75                    80                    85	
15	AAC TTA ATC TAT GCA GAT GGA AAA ACT CAA ACA GCA GAG TTC AAA GGA Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly	96
	90                    95                    100	
20	ACA TTT GCA GAA GCA ACA GCA GAA GCA TAC AGA TAC GCT GAC TTA TTA Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu	144
	105                 110                 115                 120	
25	GCA AAA GAA AAT GGT AAA TAT ACA GCA GAC TTA GAA GAT GGT GGA TAC Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr	192
	125                 130                 135	
30	ACT ATT AAT ATT AGA TTT GCA GGT Thr Ile Asn Ile Arg Phe Ala Gly	216
	140	

## 30 (2) INFORMATION FOR SEQ ID NO: 10:

35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 72 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
40	Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala 1                    5                    10                    15	80
	Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly	
	20                 25                 30	
45	Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu 35                 40                 45	
	Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr	
50	50                 55                 60	

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Thr Ile Asn Ile Arg Phe Ala Gly  
 65                           70

5

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

15

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AAA GAA ACA CCA GAA CCA GAA GAA GAA GTT ACA ATC AAA GCT AAC TTA	48
25 Lys Glu Thr Pro Glu Pro Glu Glu Val Thr Ile Lys Ala Asn Leu	
75                           80                           85	
ATC TTT GCA GAT GGA AGC ACA CAA AAT GCA GAA TTC AAA GGA ACA TTC	96
30 Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe	
90                           95                           100	
GCA AAA GCA GTA TCA GAT GCT TAC GCT GCA GAT GCT TTA AAG AAA	144
35 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys	
105                         110                         115                         120	
GAC AAC GGA GAA TAT ACT GTA GAC GTT GCA GAT AAA GGC TTA ACT TTA	192
40 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu	
125                         130                         135	
AAT ATT AAA TTC GCT GGT AAA	213
Asn Ile Lys Phe Ala Gly Lys	
140	

45

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

5 Lys Glu Thr Pro Glu Pro Glu Glu Val Thr Ile Lys Ala Asn Leu  
1 5 10 15

Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe  
20 25 30  
10 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys  
35 40 45

15 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu  
50 55 60

Asn Ile Lys Phe Ala Gly Lys  
65 70

## 20 (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

40 AAA GAA AAA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC 48  
Lys Glu Lys Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Val Asn  
75 80 85

45 TTA ATC TTT GCA GAT GGA AAG ACA CAA ACA GCA GAA TTC AAA GGA ACA 96  
Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr  
90 95 100

50 TTT GAA GAA GCA ACA GCA AAA GCT TAT GCT TAT GCA GAC TTA TTA GCA 144  
Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala  
105 110 115

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	AAA GAA AAT GGC GAA TAT ACA GCA GAC TTA GAA GAT GGT GGA AAC ACA	192
5	Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr	
	120                    125                    130 ..                    135	
	ATC AAC ATT AAA TTT GCT GGA	213
	Ile Asn Ile Lys Phe Ala Gly	
	140	
10		

## (2) INFORMATION FOR SEQ ID NO: 14:

- 15                    (i) SEQUENCE CHARACTERISTICS:  
                       (A) LENGTH: 71 amino acids  
                       (B) TYPE: amino acid  
                       (D) TOPOLOGY: linear
- 20                    (ii) MOLECULE TYPE: protein  
                       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

	Lys Glu Lys Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Val Asn	
	1                    5                    10                    15	
25	Leu Ile Phe Ala Asp Gly Lys Thr Glu Thr Ala Glu Phe Lys Gly Thr	
	20                    25                    30	
	Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala	
30	35                    40                    45	
	Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr	
	50                    55                    60	
35	Ile Asn Ile Lys Phe Ala Gly	
	65                    70	

## (2) INFORMATION FOR SEQ ID NO: 15:

- 40                    (i) SEQUENCE CHARACTERISTICS:  
                       (A) LENGTH: 222 base pairs  
                       (B) TYPE: nucleic acid  
                       (C) STRANDEDNESS: double  
                       (D) TOPOLOGY: linear
- 45                    (ii) MOLECULE TYPE: DNA (genomic)
- 50                    (ix) FEATURE:  
                       (A) NAME/KEY: CDS  
                       (B) LOCATION: 1..222

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

5	AAA GAA ACA CCA GAA ACA CCA GAA CCA AAA GAA GAA GTT ACA ATC Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile 75   80   85	48
10	AAA GTT AAC TTA ATC TTT GCA GAT GGA AAG ATA CAA ACA GCA GAA TTC Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Ile Gln Thr Ala Glu Phe 90   95   100	96
15	AAA GGA ACA TTT GAA GAA GCA ACA GCA AAA GCT TAT GCT TAT GCA AAC Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn 105   110   115	144
20	TTA TTA GCA AAA GAA AAT GGC GAA TAT ACA GCA GAC TTA GAA GAT GGT Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly 120   125   130   135	192
25	GGA AAC ACA ATC AAC ATT AAA TTT GCT GGA Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly 140   145	222

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

30	Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile 1   5   10   15
35	Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Ile Gln Thr Ala Glu Phe 20   25   30
40	Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn 35   40   45
45	Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly 50   55   60
50	Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly 65   70

## (2) INFORMATION FOR SEQ ID NO: 17:

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- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA (genomic)

- 15 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..225

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

20 AAA GAA ACA CCA GAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC  
Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile  
75 80 85 90

48

25 AAA GTT AAC TTA ATC TTT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC  
Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe  
95 100 105

96

30 AAA GGA ACA TTT GAA GAA GCA ACA GCA GAA GCT TAC AGA TAT GCA GAC  
Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp  
110 115 120

144

35 TTA TTA GCA AAA GTA AAT GGT GAA TAC ACA GCA GAC TTA GAA GAT GGC  
Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly  
125 130 135

192

40 GGA TAC ACT ATC AAC ATC AAA TTT GCT GGA AAA  
Gly Tyr Thr Ile Asn Ile Lys Phe Ala Gly Lys  
140 145

225

- 40 (2) INFORMATION FOR SEQ ID NO: 18:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

50 Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile  
1 5 10 15

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Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe  
 20 25 30

5 Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp  
 35 40 45

10 Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly  
 50 55 60

Gly Tyr Thr Ile Asn Ile Lys Phe Ala Gly Lys  
 65 70 75

15 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

30 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..246

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA 48  
 35 Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu  
 1 5 10 15

CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA 96  
 40 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly  
 20 25 30

AAG ATA CAA ACA GCA GAA CAT AAA GGA ACA TTT GAA GAA GCA ACA GCA 144  
 45 Lys Ile Gln Thr Ala Glu His Lys Gly Thr Phe Glu Glu Ala Thr Ala  
 35 40 45

GAA GCT TAC AGA TAT GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT 192  
 50 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr  
 50 55 60

50 ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT 240  
 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala  
 65 70 75 80

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GGA AAA TAA  
Gly Lys

249

5

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

20

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..246

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

25.

ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA  
Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu  
1 5 10 15

48

30

CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA  
Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly  
20 25 30

96

35

AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA  
Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala  
35 40 45

144

40

GAA GCT TAC AGA AAC GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT  
Glu Ala Tyr Arg Phe Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr  
50 55 60

192

45

GGA AAA TAA

240

Gly Lys

65 70 75 80

249

## (2) INFORMATION FOR SEQ ID NO: 21:

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

10 (B) LOCATION:1..246

(A) NAME/KEY: CDS

(B) LOCATION:1..246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

15	ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu 1 5 10 15	48
20	CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly 20 25 30	96
25	AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala 35 40 45	144
30	GAA GCT TAC AGA TAT GCA GAC TTA GAC GCA AAA GTA AAT GGC GAA TGG Glu Ala Tyr Arg Tyr Ala Asp Leu Asp Ala Lys Val Asn Gly Glu Trp 50 55 60	192
35	ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala 65 70 75 80	240
40	GGA AAA TAA Gly Lys	249

(2) INFORMATION FOR SEQ ID NO: 22:

#### 40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

50 (A) NAME/KEY: CDS  
(B) LOCATION:1..246

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

5	ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA Met Asn Ile Lys Phe Ala Gly Lys.Glu Thr Pro Glu Thr Pro Glu Glu	48
	1 5 10 15	
10	CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly	96
	20 25 30	
15	AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA Lys Ile Gln Thr Ala Glu Phe Lys Gly.Thr Phe Glu Glu Ala Thr Ala	144
	35 40 45	
20	GAA GCT TAC AGA TAT GCA GAC TTA CAT GCA AAA GTA AAT GGC GAA TAT Glu Ala Tyr Arg Tyr Ala Asp Leu His Ala Lys Val Asn Gly Glu Tyr	192
	50 55 60	
25	ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT Thr Ala Asp Leu Glu Asp Gly.Gly Asn His Met Asn Ile Lys Phe Ala	240
	65 70 75 80	
30	GGA AAA TAA Gly Lys	249
35		
40		